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Sequence Listing could not be accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=17; hr=14; min=55; sec=30; ms=563;]

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Reviewer Comments:

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<222> (1)...(1059)

<400> 2

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tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
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gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
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ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
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tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
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atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
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In a coding sequence, Per above attach please insert (3) letter codings for amino acids below the corresponding nucleotide triplets.

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown or Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. Please check for similar errors in subsequent sequences and make necessary changes.

<210>10

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> added peptide

<400> 10

Arg Leu Lys Met

Per above is an insufficient response for numeric identifier <223>. Please explain the source of the genetic material. When using "Unknown"

for numeric identifier <213>, please provide as much taxonomic information, as possible, about the organism from which the genetic material was extracted. If the genetic material was extracted from a sample in which there was an unknown variety of organisms, please explain where the sample was taken, for example a soil sample. These errors appear in other sequences in the sequence listing. Please make all necessary changes.

Application No: 10785230 Version No: 3.0

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Output Set:

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Finished: 2008-10-22 15:28:18.718
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Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

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<110> KISHIMOTO, Tadamitsu
NAGASAWA, Takashi
TACHIBANA, Kazunobu

<130> 46124-5042-US01

<140> 10785230

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<150> US 09/646,785

<151> 2001-02-16

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<151> 1998-03-24

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ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
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ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
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Phe	Lys	Ser	Ser	Ala	Gln	His	Ala	Leu	Asn	Ser	Met	Ser	Arg	Gly	
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Pro	Cys	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys
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<213> Artificial Sequence

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<220>
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          20              25              30
Pro Cys Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys
          35              40              45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
          50              55              60
Ala Arg Leu Lys Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
          65              70              75
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<211> 1781
<212> DNA
<213> Mus

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<220>
<221> CDS
<222> (82)...(351)

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81

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